

SEQUENCE LISTING

<110> APPLICANT: Novartis AG
 <120> TITLE OF INVENTION: Organic Compound
 <130> FILE REFERENCE: 4-32761P1/UNZ
 <140> CURRENT APPLICATION NUMBER: US/10/538,201
 <141> CURRENT FILING DATE: 2006-03-08
 <160> NUMBER OF SEQ ID NOS: 48
 <170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(18)
 <223> OTHER INFORMATION: rat NogoA_623-640
 <400> SEQUENCE: 1
 Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
 1 5 10 15
 Glu Ala

<210> SEQ ID NO 2
 <211> LENGTH: 221
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CHAIN
 <222> LOCATION: (1)..(221)
 <223> OTHER INFORMATION: Variable part of Heavy Chain of 11C7 with leader sequence
 <400> SEQUENCE: 2
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
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 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
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 Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
 35 40 45
 Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
 65 70 75 80
 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
 85 90 95
 Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
 100 105 110
 Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
 115 120 125
 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
 130 135 140
 Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
 145 150 155 160
 Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
 165 170 175
 Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
 180 185 190
 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
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 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 210 215 220

<210> SEQ ID NO 3
 <211> LENGTH: 238
 <212> TYPE: PRT

<213> ORGANISM: Mus musculus
 <220> FEATURE:
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 <222> LOCATION: (1)..(238)
 <223> OTHER INFORMATION: Light Chain of 11c7 with leader sequence
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 Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
 20 25 30
 Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
 35 40 45
 Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
 50 55 60
 Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
 65 70 75 80
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95
 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
 100 105 110
 Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
 130 135 140
 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
 180 185 190
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
 195 200 205
 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
 210 215 220
 Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Cys
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<210> SEQ ID NO 4
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 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(3579)
 <223> OTHER INFORMATION: Human NogoA
 <400> SEQUENCE: 4
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 ccc cgg ccg cag ccc gcg ttc aag tac cag cag gtc agg gag ccc gag 96
 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Gln Pro Glu
 20 25 30
 gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac 144
 Asp Glu Glu Glu Asp Gln Glu Glu Glu Glu Asp Glu Asp Glu Asp Glu Asp
 35 40 45
 ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc 192
 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
 50 55 60
 gcg gcc cca gtg ccc acc gcc cct gcc gcc gcc gcc gcc ctg atg gac 240
 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Ala Pro Leu Met Asp
 65 70 75 80
 ttc gga aat gac ttc gtg cgc ccg gcg gcc gcc gga ccc ctg ccg gcc 288
 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
 85 90 95

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gtg Val	tcg Ser	tcg Ser 115	gtg Thr	ccc Val	gcg Pro	cca Ala 120	ccc Ser	ccg Pro	ctg Leu	tct Ser	gct Ala 125	gcc Ala	gca Ala	gtc Val		384
tcg Ser	ccc Pro 130	ccc Pro	aag Lys	ctc Leu	cct Pro	gag Glu 135	gac Asp	gac Asp	cct Pro	ccg Pro 140	gcc Pro	cgg Arg	cct Pro	ccc Pro		432
cct Pro 145	cct Pro	ccc Pro	ccg Pro	gcc Ala	agc Val	gtg Val 150	agc Ser	ccc Pro	cag Gln	gca Ala 155	ccc Glu	gtg Val	tgg Trp	acc Thr 160		480
ccg Pro	cca Pro	gcc Pro	ccg Pro	gct Ala 165	ccc Ala	gcc Ala	gcg Ala	ccc Pro 170	ccc Pro	tcc Ser	acc Thr	ccg Pro	gcc Ala 175	gcg Pro	ccc Pro	528
aag Lys	cgc Arg	agg Arg	ggc Gly 180	tcc Ser	tcg Ser	ggc Gly	tca Ser	gtg Val 185	gat Asp	gag Glu	acc Thr	ctt Leu	ttt Phe 190	gct Ala	ctt Leu	576
cct Pro 195	gct Ala	gca Ala	tct Glu	gag Glu	cct Val	gtg Val	ata Ile 200	cgc Ser	tcc Ser	tct Ser	gca Ala 205	gaa Ala	aat Met	atg Met	gac Asp	624
ttg Leu 210	aag Glu	gag Glu	cag Gln	cca Pro	ggt Gly	aac Asn 215	act Thr	att Ile	tcg Ser	gct Ala	ggt Gly 220	caa Gln	gag Glu	gat Asp	ttc Phe	672
cca Pro 225	tct Pro	gtc Leu	ctg Leu	ctt Glu	gaa Thr 230	act Ala	gct Ala	gct Ser	tct Ser	ctt Ser	cct Ser	tct Ser	ctg Ser	tct Pro 240	cct Pro	720
ctc Leu	tca Ser	gcc Ala	gct Ala	tct Ser 245	aaa Phe	gaa Lys	cat Glu	gaa His 250	gaa Glu	tac Tyr	ggt Leu	aat Gly	ttg Asn	tca Leu 255		768
aca Thr	gta Val	tta Leu	ccc Pro 260	act Thr	gaa Glu	gga Gly	aca Thr	ctt Leu 265	caa Gln	gaa Glu	aat Asn	gtc Val	agt Ser	gaa Glu	gct Ala	816
tct Ser	aaa Thr	gag Val	gtc Val	tca Ser	gag Lys	aag Lys	gca Ala 280	aaa Lys	act Thr	cta Thr	ctc Leu	ata Ile 285	gat Ser	aga Arg	gat Asp	864
tta Leu 290	aca Glu	gag Glu	ttt Phe	tca Ser	gaa Glu	tta Leu 295	tac Glu	tca Tyr	gaa Ser	atg Met 300	gta Val	gca Ala	aat Asn	cct Pro 320	agg Arg	912
agt Ser 305	gtc Val	tct Ser	cca Pro	aaa Lys	gca Ala 310	gaa Glu	tct Ser	gcc Ala	gta Val	ata Ile 315	gta Val	gca Ala	aat Asn	cct Pro 320	agg Arg	960
gaa Glu	gaa Glu	ata Ile	atc Ile	gtg Val 325	aaa Lys	aat Asn	aaa Lys	gat Asp	gaa Glu	gag Glu	aag Lys	tta Leu	gtt Val 335	agt Ser		1008
aat Asn	aac Asn	atc Ile	ctt Leu 340	cat His	aat Gln	caa Gln	caa Gln	gag Glu 345	tta Leu	cct Pro	aca Thr	gct Ala	ctt Thr	aaa Lys		1056
ttg Leu	gtt Val	aaa Lys 355	gag Glu	gat Asp	gaa Glu	gtt Val	gtg Val 360	tct Ser	tca Ser	gaa Glu	aaa Lys	gca Ala 365	aaa Lys	gac Asp	agt Ser	1104
ttt Phe 370	aat Asn	gaa Glu	aag Glu	aga Arg	gtt Ala	gca Val 375	gtg Glu	gaa Glu	gct Ala	cct Pro	atg Met 380	agg Arg	gag Glu	gaa Glu	tat Tyr	1152
gca Ala 385	gac Asp	ttc Phe	aaa Lys	cca Pro	ttt Phe 390	gag Glu	cga Arg	gta Val	tgg Trp	gaa Glu 395	gag Val	aaa Lys	gat Asp	agt Ser	aag Lys 400	1200
gaa Glu	gat Asp	agt Asp	gat Met 405	atg Met	ttg Leu	gct Ala	gct Ala	gga Gly 410	ggt Gly	aaa Ile	atc Glu	gag Ser	agc Ser	aac Asn 415	ttg Leu	1248
gaa Glu	agt Ser	aaa Lys	gtg Val	gat Asp	aaa Lys	aaa Lys	gtg Cys	ttt Phe 425	gca Ala	gat Asp	agc Ser	ctt Leu	gag Glu	caa Gln	act Thr	1296
aat Asn	cac His	gaa Glu	aaa Lys	gat Asp	agt Ser	gag Glu	agt Ser	agt Ser	aat Asn	gat Asp	gat Asp	act Thr	tct Ser	ttc Phe	ccc Pro	1344

[illegible]

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gaa	tct	ttt	aag	ctc	agt	tta	gat	aac	aca	aaa	gat	acc	ctg	tta	cct	2448
Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	Thr	Lys	Asp	Thr	Leu	Leu	Pro	
				805					810					815		
gat	gaa	gtt	tca	aca	ttg	agc	aaa	aag	gag	aaa	att	cct	ttg	cag	atg	2496
Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys	Glu	Lys	Ile	Pro	Leu	Gln	Met	
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Glu	Leu	Ser	Thr	Ala	Val	Tyr	Ser	Ser	Asn	Asp	Asp	Leu	Phe	Ile	Ser	
				835				840				845				
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Lys	Glu	Ala	Gln	Ile	Arg	Glu	Thr	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	
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att	gaa	att	ata	gat	gag	ttc	cct	aca	ttg	atc	agt	tct	aaa	act	gat	2640
Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Leu	Ile	Ser	Ser	Lys	Thr	Asp	
					870				875						880	
tca	ttt	tct	aaa	tta	gcc	agg	gaa	tat	act	gac	cta	gaa	gta	tcc	cac	2688
Ser	Phe	Ser	Lys	Leu	Ala	Arg	Glu	Tyr	Thr	Asp	Leu	Glu	Val	Ser	His	
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aaa	agt	gaa	att	gct	aat	gcc	ccg	gat	gga	gct	ggg	tca	ttg	cct	tgc	2736
Lys	Ser	Glu	Ile	Ala	Asn	Ala	Pro	Asp	Gly	Ala	Gly	Ser	Leu	Pro	Cys	
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aca	gaa	ttg	ccc	cat	gac	ctt	tct	ttg	aag	aac	ata	caa	ccc	aaa	gtt	2784
Thr	Glu	Leu	Pro	His	Asp	Leu	Ser	Leu	Lys	Asn	Ile	Gln	Pro	Lys	Val	
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gaa	gag	aaa	atc	agt	ttc	tca	gat	gac	ttt	tct	aaa	aat	ggg	tct	gct	2832
Glu	Glu	Lys	Ile	Ser	Phe	Ser	Asp	Asp	Phe	Ser	Lys	Asn	Gly	Ser	Ala	
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aca	tca	aag	gtg	ctc	tta	ttg	cct	cca	gat	gtt	tct	gct	ttg	gcc	act	2880
Thr	Ser	Lys	Val	Leu	Leu	Leu	Pro	Pro	Asp	Val	Ser	Ala	Leu	Ala	Thr	
					950					955					960	
caa	gca	gag	ata	gag	agc	ata	gtt	aaa	ccc	aaa	gtt	ctt	gtg	aaa	gaa	2928
Gln	Ala	Glu	Ile	Glu	Ser	Ile	Val	Lys	Pro	Lys	Val	Leu	Val	Lys	Glu	
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gct	gag	aaa	aaa	ctt	cct	tcc	gat	aca	gaa	aaa	gag	gac	aga	tca	cca	2976
Ala	Glu	Lys	Leu	Pro	Ser	Pro	Ser	Thr	Glu	Lys	Glu	Asp	Arg	Ser	Pro	
					980			985					990			
tct	gct	ata	ttt	tca	gca	gag	ctg	agt	aaa	act	tca	gtt	gtt	gac	ctc	3024
Ser	Ala	Ile	Phe	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	Val	Val	Asp	Leu	
					995		1000					1005				
ctg	tac	tgg	aga	gac	att	aag	aag	act	gga	gtg	gtg	ttt	ggt	gcc		3069
Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe	Gly	Ala		
						1015					1020					
agc	cta	ttc	ctg	ctg	ctt	tca	ttg	aca	gta	ttc	agc	att	gtg	agc		3114
Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val	Ser		
						1030					1035					
gta	aca	gcc	tac	att	gcc	ttg	gcc	ctg	ctc	tct	gtg	acc	atc	agc		3159
Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser		
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ttt	agg	ata	tac	aag	ggt	gtg	atc	caa	gct	atc	cag	aaa	tca	gat		3204
Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp		
						1060					1065					
gaa	ggc	cac	cca	ttc	agg	gca	tat	ctg	gaa	tct	gaa	gtt	gct	ata		3249
Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Glu	His	Ser	Glu	Val	Ala	Ile		
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Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His		
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gtg	aac	tcg	acg	ata	aag	gaa	ctc	agg	cgc	ctc	ttc	tta	gtt	gat		3339
Val	Asn	Cys	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp		
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gat	tta	ggt	tct	ctg	aag	ttt	gca	gtg	ttg	atg	ttg	gta	ttt			3384
Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe		
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acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg	3429
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu	
1130 1135 1140	
gct ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat	3474
Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His	
1145 1150 1155	
cag gca cag ata gat cat tat cta gga ctt gca aat aag aat gtt	3519
Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val	
1160 1165 1170	
aaa gat gct atg gct aaa atc caa gca aaa atc cct gga ttg aag	3564
Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys	
1175 1180 1185	
cgc aaa gct gaa tga aaacgcccaa aataattagt aggagttcat ctttaaaggg	3619
Arg Lys Ala Glu	
1190	
gatattcatt tgattatacgc ggggagggtc aggggaagaac gaaccttgac gttgcagtc	3679
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<210> SEQ ID NO 5

<211> LENGTH: 1192

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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			20					25					30		
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Asp
			35					40				45			
Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser
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Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp
			65		70					75				80	
Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala
			85						90					95	
Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro
			100					105					110		
Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val
			115				120					125			
Ser	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	
			130			135					140				
Pro	Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr
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Pro	Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro
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Lys	Arg	Arg	Gly	Ser	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu
			180					185					190		
Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Arg	Ser	Ser	Ala	Glu	Asn	Met	Asp
			195				200					205			
Leu	Lys	Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln	Glu	Asp	Phe
			210			215					220				
Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro
			225			230				235				240	
Leu	Ser	Ala	Ala	Ser	Phe	Lys	Glu	His	Glu	Tyr	Leu	Gly	Asn	Leu	Ser
			245						250				255		
Thr	Val	Leu	Pro	Thr	Glu	Gly	Thr	Leu	Gln	Glu	Asn	Val	Ser	Glu	Ala
			260				265						270		
Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys	Thr	Leu	Leu	Ile	Asp	Arg	Asp
			275				280					285			
Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe
			290			295				300					
Ser	Val	Ser	Pro	Lys	Ala	Glu	Ser	Ala	Val	Ile	Val	Ala	Asn	Pro	Arg

305	Glu	Glu	Ile	Ile	Val	310	Lys	Asn	Lys	Asp	Glu	315	Glu	Glu	Lys	Leu	Val	320	Ser
	Asn	Asn	Ile	Leu	His	325	Asn	Gln	Gln	Glu	330	Leu	Pro	Thr	Ala	Leu	335	Thr	Lys
	Leu	Val	Lys	340	Glu	Asp	Glu	Val	Val	345	Ser	Glu	Lys	Ala	350	Lys	Asp	Ser	
	Phe	Asn	Glu	Lys	Arg	Val	Ala	360	Val	Glu	Ala	Pro	Met	365	Arg	Glu	Glu	Tyr	
	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Arg	Val	Trp	Glu	380	Val	Lys	Asp	Ser	Lys	400	
	385	Glu	Asp	Ser	Asp	Met	Leu	Ala	Ala	Gly	Gly	395	Lys	Ile	Glu	Ser	Asn	415	Leu
	Glu	Ser	Lys	Val	405	Asp	Lys	Lys	Cys	Phe	Ala	410	Asp	Ser	Leu	Glu	Gln	Thr	
	Asn	His	Glu	Lys	420	Asp	Ser	Glu	Ser	425	Asn	Asp	Asp	Thr	430	Ser	Phe	Pro	
	Ser	Thr	Pro	Glu	Gly	Ile	Lys	440	Asp	Arg	Ser	Gly	Ala	445	Tyr	Ile	Thr	Cys	
	450	Ala	Pro	Phe	Asn	Pro	Ala	455	Thr	Glu	Ser	Ile	Ala	460	Thr	Asn	Ile	Phe	
	465	Pro	Leu	Leu	Gly	Asp	Pro	Thr	Ser	Glu	Asn	475	Lys	Thr	Asp	Glu	Lys	480	
	Ile	Glu	Glu	Lys	485	Lys	Ala	Gln	Ile	Val	505	Thr	Glu	Lys	Asn	Thr	Ser	Thr	
	Lys	Thr	Ser	515	Asn	Pro	Phe	Leu	Val	520	Ala	Gln	Asp	Ser	525	Glu	Val	Ala	
	Tyr	Val	Thr	Thr	Asp	Asn	Leu	535	Thr	Lys	Val	Thr	Glu	540	Gln	Glu	Ala	Cys	
	545	Asn	Met	Pro	Glu	Gly	Leu	550	Thr	Pro	Asp	Leu	Val	555	Gln	Glu	Ala	Cys	
	Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys	570	Ile	Ala	Tyr	Glu	Thr	Lys	560	
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	Ala	Ala	Gln	595	Leu	Cys	Pro	Ser	Phe	600	Glu	Glu	Ser	Glu	Ala	605	Thr	Pro	
	Pro	Val	Leu	Pro	Asp	Ile	Val	615	Met	Glu	Ala	Pro	Leu	620	Asn	Ser	Ala	Val	
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	625	Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile	Lys	650	His	Glu	Pro	Glu	Asn	640	
	Pro	Pro	Tyr	Glu	660	Glu	Ala	Met	Ser	Val	665	Ser	Leu	Lys	Lys	670	Ser	Gly	
	Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	680	Glu	Asn	Ile	Asn	Ala	685	Ala	Leu	Gln	
	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	695	Ile	Ala	Cys	Asp	700	Leu	Ile	Lys	Glu	
	705	Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Asp	Phe	715	Ser	Asp	Tyr	Ser	Glu	
	Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	730	His	Ser	Glu	Leu	Val	735	Glu		
	Asp	Ser	Ser	Pro	740	Asp	Ser	Glu	Pro	Val	745	Asp	Leu	Phe	Ser	750	Asp	Ser	
	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	760	Asp	Glu	Thr	Val	Met	765	Leu	Val	Lys	
	Glu	Ser	Leu	Thr	Glu	Thr	Ser	775	Phe	Glu	Ser	Met	Ile	780	Glu	Tyr	Glu	Asn	
	Lys	Glu	Lys	Leu	Ser	Ala	790	Leu	Pro	Pro	Glu	Gly	795	Gly	Lys	Pro	Tyr	Leu	
	785	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	810	Lys	Asp	Thr	Leu	Leu	Pro	800	
	Asp	Glu	Val	Ser	820	Thr	Leu	Ser	Lys	Lys	825	Glu	Lys	Ile	Pro	Leu	Gln	Met	

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
 Lys Glu 835 Ala Gln Ile Arg Glu 840 Thr Glu Thr Phe Ser Asp Ser Ser Pro
 Ile Glu 850 Ile Ile Asp Glu 855 Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
 Ser Phe Ser Lys Leu 865 Ala Arg Glu Tyr Thr 875 Asp Leu Glu Val Ser His
 Lys Ser Glu Ile 885 Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
 Thr Glu Leu 900 Pro His Asp Leu Ser 905 Leu Lys Asn Ile Gln Pro Lys Val
 Glu Glu 915 Lys Ile Ser Phe Ser 920 Asp Asp Phe Ser Lys Asn Gly Ser Ala
 Thr 930 Ser Lys Val Leu Leu 935 Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
 Thr 945 Ser Lys Val Leu Leu 950 Pro Pro Asp Val Ser Ala Leu Ala Thr
 Gln Ala Glu Ile Glu 965 Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
 Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
 Ser Ala Ile 980 Phe Ser Ala Glu Leu 985 Ser Lys Thr Ser Val val Asp Leu
 Leu Tyr 995 Trp Arg Asp Ile Lys 1000 Lys Thr Gly Val val Phe Gly Ala
 Ser Leu 1010 Phe Leu Leu Leu Ser 1015 Leu Thr Val Phe Ser Ile Val Ser
 Val Thr 1025 Ala Tyr Ile Ala Leu 1030 Ala Leu Leu Ser Val Thr Ile Ser
 Phe Arg 1040 Ile Tyr Lys Gly Val 1045 Ile Gln Ala Ile Gln Lys Ser Asp
 Glu Gly 1055 His Pro Phe Arg Ala 1060 Tyr Leu Glu Ser Glu Val Ala Ile
 Ser Glu 1070 Glu Leu Val Gln Lys 1075 Tyr Ser Asn Ser Ala Leu Gly His
 Val 1085 Asn Cys Thr Ile Lys Glu 1090 Leu Arg Arg Leu Phe Leu Val Asp
 Asp Leu 1100 Val Asp Ser Leu Lys 1105 Phe Ala Val Leu Met Trp Val Phe
 Thr Tyr 1115 Val Gly Ala Leu Phe 1120 Asn Gly Leu Thr Leu Leu Ile Leu
 Ala Leu 1130 Ile Ser Leu Phe Ser 1135 Val Pro Val Ile Tyr Glu Arg His
 Gln Ala 1145 Gln Ile Asp His Tyr 1150 Leu Gly Leu Ala Asn Lys Asn Val
 Lys Asp 1160 Ala Met Ala Lys Ile 1165 Gln Ala Lys Ile Pro Gly Leu Lys
 Arg Lys 1175 Ala Glu 1180 1185

<210> SEQ ID NO 6
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(18)
 <223> OTHER INFORMATION: Human NogoA_623-640
 <400> SEQUENCE: 6
 Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
 1 5 10 15
 Glu Ala

<210> SEQ ID NO 7
 <211> LENGTH: 819
 <212> TYPE: PRT

<213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(819)
 <223> OTHER INFORMATION: human Nig
 <400> SEQUENCE: 7

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Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg
1      5      10      15
Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile
20     25     30     35     40     45
Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala
50     55     60     65     70     75     80
Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
85     90     95     100    105    110    115
Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
120    125    130    135    140    145    150
Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
155    160    165    170    175    180    185
Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
190    195    200    205    210    215    220
Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
225    230    235    240    245    250    255
Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
260    265    270    275    280    285    290
Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
295    300    305    310    315    320    325
Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
330    335    340    345    350    355    360
Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
365    370    375    380    385    390    395
Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
400    405    410    415    420    425    430
Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
435    440    445    450    455    460    465
Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
470    475    480    485    490    495    500
225 Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser
230    235    240    245    250    255    260
Asn Asp Asp Thr Ser Phe Pro Ser Thr Thr Glu Gly Ile Lys Asp Arg
265    270    275    280    285    290    295
Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
300    305    310    315    320    325    330
Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
335    340    345    350    355    360    365
Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Ala Gln Ile Val
370    375    380    385    390    395    400
Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Pro Phe Leu Val Ala
405    410    415    420    425    430    435
Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
440    445    450    455    460    465    470
Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
475    480    485    490    495    500    505
Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
510    515    520    525    530    535    540
Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val
545    550    555    560    565    570    575
385 Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
580    585    590    595    600    605    610
Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
615    620    625    630    635    640    645
Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
650    655    660    665    670    675    680
Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
685    690    695    700    705    710    715
450 Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val

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465 Ser Leu Lys Lys Val 470 Ser Gly Ile Lys Glu 475 Glu Ile Lys Glu Pro 480 Glu
 Asn Ile Asn Ala 485 Leu Gln Glu Thr 490 Glu Ala Pro Tyr Ile 495 Pro Ile
 Ala Cys Asp 500 Leu Ile Lys Glu Thr 505 Lys Leu Ser Ala Glu 510 Pro Ala Pro
 Asp Phe Ser Asp Tyr Ser Glu 515 Met Ala Lys Val Glu 525 Pro Val Pro
 Asp His Ser Glu Leu Val 530 Glu Asp Ser Ser Pro 540 Asp Ser Glu Pro Val
 545 Asp Leu Phe Ser Asp 550 Ser Ile Pro Asp 555 Val Pro Gln Lys Gln 560 Asp
 Glu Thr Val Met 565 Leu Val Lys Glu Ser 570 Leu Thr Glu Thr Ser 575 Phe Glu
 Ser Met Ile 580 Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala 590 Pro Pro
 Glu Gly Gly Lys Pro Tyr Leu 600 Ser Phe Lys Leu Ser Leu Asp Asn
 Thr 610 Lys Asp Thr Leu Leu 615 Pro Asp Glu Val Ser 620 Thr Leu Ser Lys Lys
 625 Glu Lys Ile Pro Leu 630 Met Glu Glu Leu 635 Thr Ala Val Tyr 640 Ser
 Asn Asp Asp Leu Phe 645 Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
 Thr Phe Ser Asp Ser Ser Pro Ile 665 Glu Ile Ile Asp Glu Phe Pro Thr
 Leu Ile Ser Ser Lys Thr Asp 680 Ser Phe Ser Lys Leu Ala Arg Glu Tyr
 690 Thr Asp Leu Glu Val Ser 710 His Lys Ser Glu Ile Ala Asn Ala Pro Asp
 705 Gly Ala Gly Ser Leu 725 Pro Cys Thr Glu Leu Pro His Asp Leu Ser
 Lys Asn Ile Gln 740 Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
 Phe Ser Lys Asn Gly Ser Ala Thr 760 Ser Lys Val Leu Leu Pro Pro
 Asp Val Ser Ala Leu Ala Thr 775 Gln Ala Glu Ile Glu Ser Ile Val Lys
 Pro Lys Val Leu Val Lys 790 Glu Ala Glu Lys Lys 795 Leu Pro Ser Asp Thr
 785 Glu Lys Glu Asp Arg 805 Ser Pro Ser Ala Ile 810 Phe Ser Ala Glu Leu Ser
 Lys Thr Ser

<210> SEQ ID NO 8
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 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(10)
 <223> OTHER INFORMATION: hypervariable part of heavy chain of 11C7
 <400> SEQUENCE: 8
 Gly Phe Asp Phe Arg Arg Asn Trp Met Ser
 1 5 10

<210> SEQ ID NO 9
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(17)
 <223> OTHER INFORMATION: hypervariable part of heavy chain of 11C7

<400> SEQUENCE: 9
 Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
 1 5 10 15
 Asp

<210> SEQ ID NO 10
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(9)
 <223> OTHER INFORMATION: hypervariable part of heavy chain of 11C7
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 Pro Val Trp Met Tyr Ala Met Asp Tyr
 1 5

<210> SEQ ID NO 11
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(16)
 <223> OTHER INFORMATION: hypervariable part of light chain of 11C7
 <400> SEQUENCE: 11
 Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn
 1 5 10 15

<210> SEQ ID NO 12
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(7)
 <223> OTHER INFORMATION: hypervariable part of light chain of 11C7
 <400> SEQUENCE: 12
 Leu Val Ser Lys Leu Asp Ser
 1 5

<210> SEQ ID NO 13
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: BINDING
 <222> LOCATION: (1)..(9)
 <223> OTHER INFORMATION: hypervariable part of light chain of 11C7
 <400> SEQUENCE: 13
 Trp Gln Gly Thr His Phe Pro Gln Thr
 1 5

<210> SEQ ID NO 14
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(30)
 <223> OTHER INFORMATION: DNA-CDRI-11C7
 <400> SEQUENCE: 14
 ggattcgatt ttagaagaaa ttggtgagt

<210> SEQ ID NO 15
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(51)
 <223> OTHER INFORMATION: DNA-CDR2-11C7
 <400> SEQUENCE: 15
 gaaattaatc cagatagcag taagataaac tatacgccat ctctaaagga t 51

<210> SEQ ID NO 16
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(27)
 <223> OTHER INFORMATION: DNA-CDR3-11C7
 <400> SEQUENCE: 16
 ccggtctgga tgtatgctat ggactac 27

<210> SEQ ID NO 17
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(48)
 <223> OTHER INFORMATION: DNA-CDR'1-11C7
 <400> SEQUENCE: 17
 aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat 48

<210> SEQ ID NO 18
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(21)
 <223> OTHER INFORMATION: DNA-CDR'2-11C7
 <400> SEQUENCE: 18
 ctgggtgtcta aactggactc t 21

<210> SEQ ID NO 19
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(27)
 <223> OTHER INFORMATION: DNA-CDR'3-11C7
 <400> SEQUENCE: 19
 tggcaaggta cacattttcc tcagacg 27

<210> SEQ ID NO 20
 <211> LENGTH: 54
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:

<221> NAME/KEY: CDS
 <222> LOCATION: (1)..(54)
 <223> OTHER INFORMATION: leader sequence for heavy chain of 11C7
 <400> SEQUENCE: 20
 atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc 48
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
 1 5 10 15
 cag tgt 54
 Gln Cys

<210> SEQ ID NO 21
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 21
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
 1 5 10 15
 Gln Cys

<210> SEQ ID NO 22
 <211> LENGTH: 57
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(57)
 <223> OTHER INFORMATION: leader sequence for 11C7-light chain
 <400> SEQUENCE: 22
 atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa 48
 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
 1 5 10 15
 acc agc ggt 57
 Thr Ser Gly

<210> SEQ ID NO 23
 <211> LENGTH: 19
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 23
 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
 1 5 10 15
 Thr Ser Gly

<210> SEQ ID NO 24
 <211> LENGTH: 181
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(181)
 <223> OTHER INFORMATION: human Nig-D20
 <400> SEQUENCE: 24
 Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
 1 5 10 15
 Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
 20 25 30
 Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 35 40 45
 Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
 50 55 60
 Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu

65 Ser Ile Lys His Glu Pro Glu Asn Pro Pro 75 Tyr Glu Glu Ala Met
 85 Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
 100 Asn Ile Asn Ala Ala Leu Glu Thr Glu Ala Pro Tyr Ile
 115 Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
 130 Phe Ser Asp Tyr Ser Glu Met Ala Val Glu Gln Pro
 145 Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser
 165 Phe Leu Asp Val Pro
 180

<210> SEQ ID NO 25
 <211> LENGTH: 3492
 <212> TYPE: DNA
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(3492)
 <223> OTHER INFORMATION: rat NogoA
 <400> SEQUENCE: 25

atg gaa gac ata gac cag tgc tgc ctg gtc tcc tgc tcc acg gac agc 48
 Met Glu Asp Ile Asp Gln Ser Ser Leu Val 10 Ser Ser Ser Thr Asp Ser
 1 cgc gcc cgc cct cgc gcc gcc ttc aag tac cag ttc gtg acg gag gcc 96
 Pro Pro Arg Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
 20 gag gac gag gag gac gag gag gag gag gag gag gag gag gag 144
 Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
 35 gac gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192
 Glu Asp Leu Glu Glu Leu Glu Val Glu Leu Glu Arg Lys Pro Ala Ala Gly
 50 ctg tcc gca gct gcg gtg cgc gcc gcc gcc gcc gcc gcc cgc ctg ctg gac 240
 Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Ala Ala Ala Asp
 65 ttc agc agc gac tgc ctg ccc ccc gcg ccc cgc ggg cgc ctg cgc gcc 288
 Phe Ser Ser Asp Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
 85 gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc 336
 Ala Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
 100 gcg gcg ccc gcg cca tcc ctg cgc gcc gca gtc cgc ctg ccc tcc 384
 Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
 115 aag ctg cca gag gac gac gag cct cgc gcg agg ccc cgc cct cgc ccg 432
 Leu Leu Pro Glu Asp Glu Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro
 130 cca gcc gcc gcg agc ccc ctg gcg gag gcc gcc gcg gcc cct tcc acg 480
 Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
 145 cgc gcc gcg ccc aag gcg agg gcc tcc gcc tca gtg gat gag acc ctt 528
 Pro Glu Ala Pro Lys Arg Arg Gly Ser Val Asp Glu Thr Thr Leu
 165 ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa 576
 Phe Ala Leu Pro Ala Ala Ser Glu Val Ile Pro Ser Ser Ala Glu
 180 aaa att atg gat ttg atg gag cag cca ggt aac act gtt tgc tct ggt 624
 Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
 195 caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct 672

Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	
210	210					215					220					
tct	cta	tct	cct	ctc	tca	act	gtt	tct	ttt	aaa	gaa	cat	gga	tac	ctt	720
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu	
225					230					235					240	
ggt	aac	tta	tca	gca	gtg	tca	tcc	tca	gaa	gga	aca	att	gaa	gaa	act	768
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	Thr	
				245					250					255		
tta	aat	gaa	gct	tct	aaa	gag	ttg	cca	gag	agg	gca	aca	aat	cca	ttt	816
Leu	Asn	Glu	Ala	Ser	Glu	Glu	Leu	Pro	Arg	Ala	Thr	Thr	Pro	Pro	Phe	
				260				265					270			
gta	aat	aga	gat	tta	gca	gaa	ttt	tca	gaa	tta	gaa	tat	gaa	atg		864
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	
		275					280					285				
gga	tca	tct	ttt	aaa	ggc	tcc	cca	aaa	gga	gag	tca	gcc	ata	tta	gta	912
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Gly	Gly	Arg	Glu	Ala	Ile	Leu	Val	
	290				295						300					
gaa	aac	act	aag	gaa	gaa	gta	att	gtg	agg	agt	aaa	gac	aaa	gag	gat	960
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	
305					310					315				320		
tta	gtt	tgt	agt	gca	gcc	ctt	cac	agt	cca	caa	gaa	tca	cct	gtg	ggt	1008
Leu	Ser	Ser	Ser	Ala	Leu	His	His	Ser	Glu	Glu	Ser	Ala	Pro	Val	Gly	
				325					330					335		
aaa	gaa	gac	aga	gtt	gtg	tct	cca	gaa	aag	aca	atg	gac	att	ttt	aat	1056
Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	
				340				345					350			
gaa	atg	cag	atg	tca	gta	gta	gca	cct	gtg	agg	gaa	gag	tat	gca	gac	1104
Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Glu	Glu	Glu	Tyr	Ala	asp	
	355						360				365					
ttt	aag	cca	ttt	gaa	caa	gca	tgg	gaa	gtg	aaa	gat	act	tat	gag	gga	1152
Phe	Gly	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	
	370					375					380					
agt	agg	gat	gtg	ctg	gct	gct	aga	gct	aat	gtg	gaa	agt	aaa	gtg	gac	1200
Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp	
385					390				395					400		
aga	aaa	tgc	ttg	gaa	gat	agc	ctg	gag	caa	aaa	agt	ctt	ggg	aag	gat	1248
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp	
				405				410					415			
agt	gaa	ggc	aga	aat	gag	gat	gct	tct	ttc	ccc	agt	acc	cca	gaa	cct	1296
Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Thr	Glu	Pro	
				420				425					430			
gtg	aag	gac	agc	tcc	aga	gca	tat	att	acc	tgt	gct	tcc	phe	acc	tca	1344
Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Thr	Thr	Ser	
		435					440				445					
gca	acc	gaa	agc	acc	aca	gca	aac	act	ttc	cct	ttg	tta	gaa	gat	cat	1392
Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His	
		450				455					460					
act	tca	gaa	aat	aaa	aca	gat	gaa	aaa	aaa	ata	gaa	gaa	agg	aag	gcc	1440
Thr	Ser	Gln	Lys	Lys	Thr	Asp	Glu	Lys	Ile	Glu	Glu	Thr	Asp	Lys	Ala	
465					470				475					480		
caa	att	ata	aca	gag	act	agc	ccc	aaa	acg	tca	aat	cct	ttc	ctt		1488
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Thr	Ser	Asn	Pro	Phe	Leu		
				485				490					495			
gta	gca	gta	cag	gat	tct	gag	gca	gat	tat	gtt	aca	aca	gat	acc	tta	1536
Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Thr	Thr	Thr	Thr	Asp	Thr	Leu	
			500					505					510			
tca	aag	gtg	act	agc	gca	gca	gtg	tca	aac	atg	cct	gaa	ggc	ctg	acg	1584
Ser	Lys	Val	Thr	Thr	Glu	Ala	Ala	Val	Asn	Met	Pro	Glu	Gly	Leu	Thr	
		515					520					525				
cca	gat	tta	gtt	cag	gaa	gca	tgt	gaa	agt	gaa	ctg	aat	gaa	gcc	aca	1632
Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Leu	Ala	Asn	Glu	Ala	Thr	
		530				535					540					
ggt	aca	aag	att	gct	tat	gaa	aca	aaa	gtg	gac	ttg	gtc	caa	aca	tca	1680
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser	
545					550					555					560	

gaa Glu	gct Ala	ata Ile	caa Gln	gaa Glu 565	tca Ser	ctt Leu	tac Tyr	ccc Pro	aca Thr 570	gca Ala	cag Gln	ctt Leu	tgc Cys	cca Pro 575	tca Ser	1728
ttt Phe	gag Glu	gaa Glu	gct Ala 580	gaa Glu	gca Ala	act Thr	ccg Pro	tca Ser 585	ggt Pro	ttg Val	cct Pro	gat Ala 590	att Ile	gtt Val		1776
atg Met	gaa Glu 595	gca Ala	cca Pro	tta Leu	aat Asn	tct Ser	ctc Leu 600	ctt Leu	cca Pro	agc Ser	gct Ala 605	ggg Gly 610	gct Ala	tct Ser	gta Val	1824
gtg Val	cag Gln 610	ccc Pro	agt Ser	gta Val	tcc Ser	cca Pro 615	ctg Leu	gaa Glu	gca Ala	cct Pro	cct Pro 620	cca Pro	ggt Val	agt Ser	tat Tyr	1872
gac Asp 625	agt Ser	ata Ala	aag Leu	ctt Leu	gag Glu 630	cct Pro	gaa Glu	aac Asn	ccc Pro	cca Pro 635	cca Pro	tat Tyr	gaa Glu	gaa Glu	gcc Ala 640	1920
atg Met	aat Asn	gta Val	gca Ala	cta Leu 645	aaa Lys	gct Ala	ttg Leu	gga Gly	aca Thr 650	aag Lys	gaa Glu	gga Gly	ata Ile	aaa Lys 655	gag Glu	1968
cct Pro	gaa Glu	agt Phe	ttt Asn 660	aat Asn	gca Ala	gct Ala	gtt Val	cag Gln 665	gaa Glu	aca Thr	gaa Glu	gct Ala 670	cct Tyr	tat Ser	ata Ile	2016
tcc Ser	att Ile	gcg Ala 675	tgt Cys	gat Asp	tta Leu	att Ile	aaa Lys 680	gaa Glu	aca Thr	aag Lys	ctc Leu	tcc Ser 685	act Thr	gag Glu	cca Pro	2064
agt Ser 690	cca Pro	gat Phe	ttc Ser	tct Asn	aat Tyr	tat Tyr 695	tca Ser	gaa Glu	ata Ile	gca Ala	aaa Lys 700	ttc Phe	gag Glu	aag Ser	tcg Ser	2112
gtg Val 705	ccc Pro	gaa Glu	cac His	gct Ala	gag Glu 710	cta Leu	gtg Val	gag Glu	tcc Ser 715	gca Ala	cct Ser	gaa Pro	tct Glu	gaa Ser	gaa Glu 720	2160
cca Pro Val	gtt Asp	gac Leu	tta Leu	ttt Ser 725	agt Ser	gat Asp	gat Asp	tcg Ser	att Pro	cct Pro	gaa Glu	gtc Val	cca Pro	caa Gln 735	aca Thr	2208
caa Gln	gag Glu	gag Ala 740	gct Val	gtg Val	atg Met	ctc Leu	aag Met	gag Lys 745	gag Glu	agt Ser	ctc Leu	act Thr	gaa Glu 750	gtg Val	tct Ser	2256
gag Glu	aca Thr 755	gta Ala	gcc Ala	cag Gln	cac His	aaa Lys	gag Glu 760	aga Arg	ctt Leu	agt Ser	gcc Ala 765	act Ser	cct Pro	cag Gln		2304
gag Glu 770	cta Leu	gga Gly	aag Lys	cca Pro	tat Tyr	tta Leu 775	gag Glu	tct Ser	ttt Phe	cag Gln	ccc Pro 780	aat Asn	tta Leu	cat His	agt Ser	2352
aca Thr 785	aaa Lys	gat Asp	gct Ala	gca Ala	tct Ser 790	aat Asn	gac Asp	att Ile	cca Pro	aca Thr 795	acc Leu	aaa Lys	aag Lys	gag Glu 800		2400
aaa Lys	att Ser	tct Leu	ttg Gln 805	caa Met	atg Glu	gaa Glu	gag Glu	ttt Phe 810	aat Asn	act Thr	gca Ala	att Ile	tat Tyr	tca Ser 815	aat Asn	2448
gat Asp	gac Asp	tta Leu	ctt Leu 820	tct Ser	tct Ser	aag Lys	gaa Glu	gac Asp 825	aaa Lys	ata Ile	aaa Lys	gaa Glu	agt Ser 830	gaa Glu	aca Thr	2496
ttt Phe	tca Ser	gat Ser	tca Ser	tct Ser	ccg Pro	att Ile	gag Glu 840	ata Ile	ata Ile	gat Asp	gaa Glu	ttt Pro 845	ccc Pro	acg Thr	ttt Phe	2544
gtc Val	agt Ser 850	gct Ala	aaa Lys	gat Asp	gat Asp	tct Ser 855	cct Pro	aaa Lys	tta Leu	gcc Ala	aag Lys 860	gag Glu	tac Tyr	act Thr	gat Asp	2592
cta Leu 865	gaa Glu	gta Val	tcc Ser	gac Lys	aaa Ser	agt Glu 870	gaa Glu	att Ile	gct Ala	aat Ile	atc Gln	caa Ser	agc Ser	ggg Gly	gca Ala 880	2640
gat Asp	tca Ser	ttg Leu	cct Pro	tcg Cys 885	tta Leu	gaa Glu	ttg Leu	ccc Pro	tgt Cys	gac Asp	ctt Leu	tct Ser	ttc Phe	aat Lys 895	aat Asn	2688
ata Ile	tat Tyr	cct Pro	aaa Lys	gat Asp	gaa Glu	gta Val	cat His	gtt Val	tca Ser	gat Asp	gaa Glu	ttc Phe	tcc Ser	gaa Glu	aat Asn	2736

			900					905				910					
agg	tcc	agt	gta	tct	aag	gca	tcc	ata	tcg	cct	tca	aat	gtc	tct	gct		2784
Arg	Ser		Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	Val	Ser	Ala		
			915				920					925					
ttg	gaa	cct	cag	aca	gaa	atg	ggc	agc	ata	gtt	aaa	tcc	aaa	tca	ctt		2832
Leu	Glu	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser	Lys	Ser	Leu		
	930					935					940						
acg	aaa	gaa	gca	gag	aaa	aaa	ctt	cct	tct	gac	gag	gag	aaa	gag	gac		2880
Thr	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp		
	945				950					955				960			
aga	tcc	ctg	tca	gct	gta	ttg	tca	gca	gag	ctg	agt	aaa	act	tca	gtt		2928
Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	Val		
				965					970					975			
gtt	gac	ctc	ctc	tac	tggt	aga	gac	att	aag	act	gga	gtg	gtg	ttt		2976	
Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Phe			
			980					985				990					
ggt	gcc	agc	tta	ttc	ctg	ctg	ctg	tct	ctg	aca	gtg	ttc	agc	att	gtc		3024
Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Phe	Ser	Leu	Thr	Val	Ser	Ile	Val		
			995				1000					1005					
agt	gta	acg	gcc	tac	att	gcc	ttg	gcc	ctg	ctc	tcg	gtg	act	atc		3069	
Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile			
	1010					1015					1020						
agc	ttt	agg	ata	tat	aag	ggc	gtg	atc	cag	gct	atc	cag	aaa	tca		3114	
Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser			
	1025					1030					1035						
gat	gaa	ggc	cac	cca	ttc	agg	gca	tat	tta	gaa	tct	gaa	lyt	gct		3159	
Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala			
	1040					1045					1050						
ata	tca	gag	gaa	ttg	gtt	cag	aaa	tac	agt	aat	tct	gct	ctt	ggt		3204	
Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly			
	1055					1060					1065						
cat	gtg	aac	agc	aca	ata	aaa	gaa	ctg	agg	cgg	ctt	ttc	tta	gtt		3249	
His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val			
	1070					1075					1080						
gat	gat	tta	gtt	gat	tcc	ctg	aag	ttt	gca	gtg	ttg	atg	tggt	gtg		3294	
Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val			
	1085					1090					1095						
ttt	act	tat	gtt	ggt	gcc	ttg	ttc	aat	ggt	ctg	aca	cta	ctg	att		3339	
Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile			
	1100					1105					1110						
tta	gct	ctg	atc	tca	ctc	ttc	agt	att	cct	gtt	att	tat	gaa	cgg		3384	
Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg			
	1115					1120					1125						
cat	cag	gtg	cag	ata	gat	cat	tat	cta	gga	ctt	gca	aac	aag	agt		3429	
His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala	Asn	Lys	Ser			
	1130					1135					1140						
gtt	aag	gat	gcc	atg	gcc	aaa	atc	caa	gca	aaa	atc	cct	gga	ttg		3474	
Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro	Gly	Leu			
	1145					1150					1155						
aag	cgc	aaa	gca	gat	tga											3492	
Lys	Arg	Lys	Ala	Asp													
	1160																

<210> SEQ ID NO 26

<211> LENGTH: 1163

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 26

Met	Glu	Asp	Ile	Asp	Gln	Ser	Ser	Leu	Val	Ser	Ser	Ser	Thr	Asp	Ser
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Pro	Pro	Arg	Pro	Pro	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Thr	Glu	Pro
			20					25					30		
Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Asp
		35					40					45			

Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly
50	50					55					60				
Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala	Pro	Leu	Leu	Asp	
65					70				75					80	
Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala
			85						90					95	
Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro
			100					105				110			
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser
			115					120				125			
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro
	130					135					140				
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr
145					150					155					160
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu
				165				170						175	
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu
			180					185					190		
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly
		195					200					205			
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro
	210					215					220				
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu
225					230					235					240
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	Thr
				245					250					255	
Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe
			260					265					270		
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met
		275					280					285			
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val
	290					295					300				
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp
305					310					315					320
Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly
				325					330					335	
Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn
			340					345					350		
Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp
	355						360					365			
Phe	Lys	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly
	370					375					380				
Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp
385					390					395				400	
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp
				405					410					415	
Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro
			420					425					430		
Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser
		435					440					445			
Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His
	450					455					460				
Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala
465					470					475					480
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe	Leu
				485					490					495	
Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp	Thr	Leu
			500					505					510		
Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr
		515					520					525			
Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr
	530					535					540				
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser
545					550					555				560	
Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser

Phe	Glu	Glu	Ala	565	Thr	Pro	Ser	570	Val	Leu	Pro	Asp	575
Met	Glu	Ala	580	Glu	Ala	Thr	Pro	Ser	585	Pro	Val	Leu	Pro
Val	Gln	Pro	Ser	Val	Ser	Pro	Glu	Ala	Pro	Pro	Gly	Ala	Ser
Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Tyr	Glu	Glu
Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile
Pro	Glu	Ser	Phe	660	Asn	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro
Ser	Ile	Ala	Cys	675	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser
Ser	Pro	Asp	Phe	690	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	700
Val	Pro	Glu	His	Ala	Glu	Val	Glu	Asp	Ser	715	Ser	Pro	Glu
Pro	Val	Asp	Leu	Phe	725	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val
Gln	Glu	Glu	Ala	740	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr
Glu	Thr	Val	Ala	755	Gln	His	Lys	Glu	760	Arg	Leu	Ser	Ala
Glu	Leu	Gly	Lys	Pro	Tyr	Leu	775	Ser	Phe	Gln	Pro	780	Asn
Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr	795	Leu	Thr
Thr	Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	810	Lys	Thr
Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	825	Lys	Ile	Lys	Glu
Phe	Ser	Asp	835	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	845
Val	Ser	Ala	Lys	Asp	Asp	Ser	855	Pro	Lys	Leu	Ala	Lys	860
Leu	Glu	Val	Ser	Asp	Lys	870	Glu	Leu	Pro	Cys	885	Asp	Leu
Asp	Ser	Leu	Pro	Cys	885	Leu	Glu	Leu	Pro	Cys	890	Ser	Asp
Ile	Tyr	Pro	Lys	900	Asp	Val	His	Val	905	Ser	Asp	Glu	Phe
Arg	Ser	Ser	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	925
Leu	Glu	Pro	Gln	Thr	Glu	Met	935	Gly	Ser	Ile	Val	Lys	940
Thr	Lys	Glu	Ala	Glu	Lys	950	Lys	Leu	Pro	Ser	Asp	955	Thr
Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr
Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val
Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	1005
Ser	Val	Thr	Ala	Tyr	Ile	Ala	1015	Leu	Ala	Leu	Leu	Ser	1020
Ser	Phe	Arg	Ile	Tyr	Lys	Gly	1030	Val	Ile	Gln	Ala	Ile	1035
Asp	Glu	Gly	His	Pro	Phe	Arg	1045	Ala	Tyr	Leu	Glu	Ser	1050
Ile	Ser	Glu	Glu	Leu	Val	Gln	1060	Lys	Tyr	Ser	Asn	Ser	1065
His	Val	Asn	Ser	Thr	Ile	Lys	1075	Glu	Leu	Arg	Arg	Leu	1080

Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val
1085						1090					1095			
Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile
1100						1105					1110			
Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg
1115						1120					1125			
His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala	Asn	Lys	Ser
1130						1135					1140			
Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro	Gly	Leu
1145						1150					1155			
Lys	Arg	Lys	Ala	Asp										
1160														

<210> SEQ ID NO 27
 <211> LENGTH: 25
 <212> TYPE: PRT
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(25)
 <223> OTHER INFORMATION: rat PEP4
 <400> SEQUENCE: 27
 Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn
 1 5 10 15
 Ser Thr Ile Lys Glu Leu Arg Arg Leu
 20 25

<210> SEQ ID NO 28
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PRO/SER rich peptide
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)..(17)
 <223> OTHER INFORMATION: Synthetic peptide
 <400> SEQUENCE: 28
 Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
 1 5 10 15
 Ser

<210> SEQ ID NO 29
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: CA-NA-2F
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(25)
 <223> OTHER INFORMATION: CA-NA-2F primer
 <400> SEQUENCE: 29
 aagcaccatt gaattctgca gtctc

25

<210> SEQ ID NO 30
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

<223> OTHER INFORMATION: CA-NA-3R
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(28)
 <223> OTHER INFORMATION:
 <400> SEQUENCE: 30
 aactgcagta ctgagctcct ccatctgc

28

<210> SEQ ID NO 31
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: forward 5'
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(33)
 <223> OTHER INFORMATION: forward primer
 <400> SEQUENCE: 31
 gtgcgggatac catggagacc ctttttgctc ttc

33

<210> SEQ ID NO 32
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: reverse 5'
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(27)
 <223> OTHER INFORMATION: reverse primer
 <400> SEQUENCE: 32
 gttctcgagt tatgaagttt tactcag

27

<210> SEQ ID NO 33
 <211> LENGTH: 29
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: forward 5'-1
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(29)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 33
 gtgcggatcc atggatttga aggagcagc

29

<210> SEQ ID NO 34
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: reverse 5'-1
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(28)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 34
 gtttctcgag tgaagtttta ttcagctc

28

<210> SEQ ID NO 35

<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5' primer
<220> FEATURE:
<221> NAME/KEY: primer_bind
<222> LOCATION: (1)..(20)
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 35
tccacccccg ccgcgcccaa 20

<210> SEQ ID NO 36
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5' primer 2
<220> FEATURE:
<221> NAME/KEY: primer_bind
<222> LOCATION: (1)..(22)
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 36
aatgatgggc aaagctgtgc tg 22

<210> SEQ ID NO 37
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 3' primer
<220> FEATURE:
<221> NAME/KEY: primer_bind
<222> LOCATION: (1)..(24)
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 37
ggtacaaga ttgcttatga aaca 24

<210> SEQ ID NO 38
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 3' primer 2
<220> FEATURE:
<221> NAME/KEY: primer_bind
<222> LOCATION: (1)..(22)
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 38
agcaggcca aggcaatgta gg 22

<210> SEQ ID NO 39
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5'-VL leader
<220> FEATURE:
<221> NAME/KEY: primer_bind
<222> LOCATION: (1)..(28)

<223> OTHER INFORMATION: primer
 <400> SEQUENCE: 39
 aatatgagtc ctgcccagtt cctgtttc 28

<210> SEQ ID NO 40
 <211> LENGTH: 32
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 3'-Ck
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(32)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 40
 ttaggaattc ctaacactct cccctgttga ag 32

<210> SEQ ID NO 41
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5'-VH leader
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(31)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 41
 aatatggatt ttgggctgat tttttttatt g 31

<210> SEQ ID NO 42
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 3'-CH hinge
 <220> FEATURE:
 <221> NAME/KEY: primer_bind
 <222> LOCATION: (1)..(24)
 <223> OTHER INFORMATION: primer
 <400> SEQUENCE: 42
 aattgggcaa cgttgcaggt gacg 24

<210> SEQ ID NO 43
 <211> LENGTH: 663
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_binding
 <222> LOCATION: (1)..(663)
 <223> OTHER INFORMATION: DNA variable part of heavy chain 11C7
 <400> SEQUENCE: 43
 atggattttg ggctgatttt ttttattgtt ggtcttttaa aaggggtcca gtgtgaggtg 60
 aaagcttctcg agtctggagg tggcctgggt cagcctggag gatccctgaa actctcctgt 120
 gtagtctcag gattcgattt tagaagaaat tggatgagtt gggctcggca ggctcctggg 180
 aaagggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgcca 240
 tctctaaagg ataaattcat catctccaga gacaatgcca agaatacgct gtacctgcaa 300
 gtgagcacag tgagattctga ggacacagcc ctttattact gtgtgagacc ggtctggatg 360
 tatgtattgg actactgggg tcaaggaacc tcagtcaccg tctctcagc caaaacgaca 420
 ccccatctg tctatccact ggcccttggg tctgctgcc aaactaact catggtgacc 480
 ctgggatgcc tgggtcaagg ctatttcctt gaggcagtg cagtgacctg gaactctgga 540

tcctctgtcca	gcgggtgtgca	caccttccca	gctgtctctgc	agtctgacct	ctacactctg	600
agcagctcag	tgactgtccc	ctccagcacc	tggcccacag	agaccgtcac	ctgcaacgtt	660
gcc						663

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<210> SEQ ID NO 44
<211> LENGTH: 717
<212> TYPE: DNA
<213> ORGANISM: Mus musculus
<220> FEATURE:
<221> NAME/KEY: misc_binding
<222> LOCATION: (1)..(717)
<223> OTHER INFORMATION: variable part of light chain of 11C7
<400> SEQUENCE: 44
atgagtctctg cccagttctct gtttctgtta gtgctctgga ttggggaac cagcgggtgat 60
gttctgttga cccagactcc tctcactttg tcgataacca ttggacaacc agcctccatc 120
tcttgcaggt caagtcagag cctcttgcac agtgaatgaa agacatatat gaattgggtg 180
ttacagaggc caggccagtc tccaaagcgc ctaatctatc ttggtgtctaa actggactct 240
ggagtccctg acaggttcac tggcagtgga tcagggaagg atttcacact gaaaatcagc 300
agagtggagg ctgaggatttt gggactttat tattgtctgc aaggtacaca ttttcctcag 360
acgttccggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420
attctccacc catccagtga gcagttaaca tctggagggt cctcagtcgt gtcgttcttg 480
aacaacttct accccaaaga catcaatgtc aagtgggaaga ttgatggcag tgaacgacaa 540
aatggcgctc tgaacagttg gactgatcag gacagcaaa acagcaccta cagcatgagc 600
agcaccttca cgttgaccac ggacgagtat gaacgacata acagctatac ctgtgaggcc 660
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag 717

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<210> SEQ ID NO 45
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 45
Thr Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45
Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
50 55 60
Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80
Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
85 90 95
Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110
Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
115 120 125
Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140
Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175
Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190
Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220

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Gln Asp Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr
225 230 235

<210> SEQ ID NO 46
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Pan paniscus
<400> SEQUENCE: 46

Gly Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25 30
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45 50
Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
55 60 65
Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
70 75 80
Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Ala
85 90 95
Val Gln Pro Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110
Ser Ile Ile His Glu Pro Glu Asn Pro Pro Tyr Glu Glu Ala Met
115 120 125
Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140
Pro Glu Ser Ile Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175
Thr Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190
Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220
Gln Asp Glu Ala Val Met Leu Val Lys Glu Asn Leu Pro Glu Thr
225 230 235

<210> SEQ ID NO 47
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus
<400> SEQUENCE: 47

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
1 5 10 15
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
20 25 30
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
35 40 45 50
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
55 60 65
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
70 75 80
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
85 90 95
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
100 105 110
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
115 120 125
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
130 135 140
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile

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<210> SEQ ID NO 48
<211> LENGTH: 239
<212> TYPE: PRT
<213> Mus musculus
<400> SEQUENCE: 48
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SEQUENCE 1	Val	Thr	Glu	Ala	Val	Val	Ala	Thr	Met	Pro	Glu	Gly	Leu	Thr
Pro	Lys	Leu	Val	Gln	Glu	Ala	Cys	Glu	Glu	Leu	Asn	Glu	Ala	Thr
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Val	Asp	Leu	Val	Gln	Thr	Ser
Glu	Ala	Ile	Gln	Glu	Ser	Ile	Thr	Pro	Thr	Ala	Gln	Leu	Cys	Pro
Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile
Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Val	Ser	Thr	Gly	Ala
Ala	Gln	Pro	Ser	Ala	Ser	Pro	Leu	Glu	Val	Pro	Ser	Pro	Val	Ser
Asp	Gly	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Ala
Met	Ser	Val	Ala	Leu	Lys	Thr	Ser	Asp	Ser	Lys	Glu	Glu	Ile	Lys
Pro	Glu	Ser	Phe	Asn	Ala	Ala	Ala	Gln	Glu	Ala	Glu	Ala	Pro	Tyr
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu
Ser	Pro	Glu	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys
Val	Pro	Asp	His	Cys	Glu	Leu	Val	Asp	Asp	Ser	Ser	Pro	Glu	Ser
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln
Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	Glu	Val